



IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/891,119B

DATE: 10/01/2004

TIME: 11:47:22

Input Set : A:\24577-cyb.ST25.txt
 Output Set: N:\CRF4\10012004\I891119B.raw

3 <110> APPLICANT: Maddon, Paul J.
 5 <120> TITLE OF INVENTION: DERIVATIVES OF SOLUBLE T-4
 7 <130> FILE REFERENCE: 24577-CY-B
 9 <140> CURRENT APPLICATION NUMBER: 09/891,119B
 10 <141> CURRENT FILING DATE: 2001-06-25
 12 <160> NUMBER OF SEQ ID NOS: 22
 14 <170> SOFTWARE: PatentIn version 3.1
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 1273
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Human
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 22 <221> NAME/KEY: CDS
 23 <222> LOCATION: (76)..(1257)
 24 <223> OTHER INFORMATION:
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 29 <222> LOCATION: (1261)..(1269)
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 37 Met Asn Arg Gly Val Pro Phe Arg His Leu Leu Leu
 38 1 5 10
 40 gtg ctg caa ctg gcg ctc ctc cca gca gcc act cag gga aag aaa gtg 159
 41 Val Leu Gln Leu Ala Leu Leu Pro Ala Ala Thr Gln Gly Lys Lys Val
 42 15 20 25
 44 gtg ctg ggc aaa aaa ggg gat aca gtg gaa ctg acc tgt aca gct tcc 207
 45 Val Leu Gly Lys Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser
 46 30 35 40
 48 cag aag agc ata caa ttc cac tgg aaa aac tcc aac cag ata aag 255
 49 Gln Lys Lys Ser Ile Gln Phe His Trp Lys Asn Ser Asn Gln Ile Lys
 50 45 50 55 60
 52 att ctg gga aat cag ggc tcc tcc tta act aaa ggt cca tcc aag ctg 303
 53 Ile Leu Gly Asn Gln Gly Ser Ser Leu Thr Lys Gly Pro Ser Lys Leu
 54 65 70 75
 56 aat gat cgc gct gac tca aga aga agc ctt tgg gac caa gga aac ttc 351
 57 Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe
 58 80 85 90
 60 ccc ctg atc atc agg aat ctt aag ata gaa gac tca gat act tac atc 399
 61 Pro Leu Ile Ile Arg Asn Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile
 62 95 100 105
 64 tgt gaa gtg gag gac cag gag gag gtg caa ttg cta gtg ttc gga 447

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65	Cys	Glu	Val	Glu	Asp	Gln	Lys	Glu	Glu	Val	Gln	Leu	Leu	Val	Phe	Gly	
66	110							115				120					
68	ttg	act	gcc	aac	tct	gac	acc	cac	ctg	ctt	cag	ggg	cag	agc	ctg	acc	495
69	Leu	Thr	Ala	Asn	Ser	Asp	Thr	His	Leu	Leu	Gln	Gly	Gln	Ser	Leu	Thr	
70	125							125				135			140		
72	ctg	acc	ttg	gag	agc	ccc	cct	ggt	agt	agc	ccc	tca	gtg	caa	tgt	agg	543
73	Leu	Thr	Leu	Glu	Ser	Pro	Pro	Gly	Ser	Ser	Pro	Ser	Val	Gln	Cys	Arg	
74								145			150			155			
76	agt	cca	agg	ggt	aaa	aac	ata	cag	ggg	ggg	aag	acc	ctc	tcc	gtg	tct	591
77	Ser	Pro	Arg	Gly	Lys	Asn	Ile	Gln	Gly	Gly	Lys	Thr	Leu	Ser	Val	Ser	
78								160			165			170			
80	cag	ctg	gag	ctc	cag	gat	agt	ggc	acc	tgg	aca	tgc	act	gtc	ttg	cag	639
81	Gln	Leu	Glu	Leu	Gln	Asp	Ser	Gly	Thr	Trp	Thr	Cys	Thr	Val	Leu	Gln	
82								175			180			185			
84	aac	cag	aag	gtg	gag	ttc	aaa	ata	gac	atc	gtg	gtg	cta	gct	ttc		687
85	Asn	Gln	Lys	Lys	Val	Glu	Phe	Lys	Ile	Asp	Ile	Val	Val	Leu	Ala	Phe	
86								190			195			200			
88	cag	aag	gcc	tcc	agc	ata	gtc	tat	aag	aaa	gag	ggg	gaa	cag	gtg	gac	735
89	Gln	Lys	Ala	Ser	Ser	Ile	Val	Tyr	Lys	Glu	Gly	Glu	Gln	Val	Asp		
90	205							205			210			215			220
92	ttc	tcc	ttc	cca	ctc	gcc	ttt	aca	gtt	gaa	aag	ctg	acg	ggc	agt	ggc	783
93	Phe	Ser	Phe	Pro	Leu	Ala	Phe	Thr	Val	Glu	Lys	Leu	Thr	Gly	Ser	Gly	
94								225			230			235			
96	gag	ctg	tgg	tgg	cag	gcg	gag	agg	gct	tcc	tcc	aag	tct	tgg	atc		831
97	Glu	Leu	Trp	Trp	Gln	Ala	Glu	Arg	Ala	Ser	Ser	Ser	Lys	Ser	Trp	Ile	
98								240			245			250			
100	acc	ttt	gac	ctg	aag	aac	aag	gaa	gtg	tct	gtt	aaa	ccg	gtt	acc	cag	879
101	Thr	Phe	Asp	Leu	Lys	Asn	Lys	Glu	Val	Ser	Val	Lys	Arg	Val	Thr	Gln	
102								255			260			265			
104	gac	cct	aag	ctc	cag	atg	ggc	aag	aag	ctc	ccg	ctc	cac	ctc	acc	ctg	927
105	Asp	Pro	Lys	Leu	Gln	Met	Gly	Lys	Lys	Leu	Pro	Leu	His	Leu	Thr	Leu	
106								270			275			280			
108	ccc	cag	gcc	ttg	cct	cag	tat	gct	ggc	tct	gga	aac	ctc	acc	ctg	gcc	975
109	Pro	Gln	Ala	Leu	Pro	Gln	Tyr	Ala	Gly	Ser	Gly	Asn	Leu	Thr	Leu	Ala	
110	285							285			290			295			300
112	ctt	gaa	gcf	aaa	aca	gga	aag	ttg	cat	cag	gaa	gtg	aac	ctg	gtg	gtg	1023
113	Leu	Glu	Ala	Lys	Thr	Gly	Lys	Leu	His	Gln	Glu	Val	Asn	Leu	Val	Val	
114								305			310			315			
116	atg	aga	gcc	act	cag	ctc	cag	aaa	aat	ttg	acc	tgt	gag	gtg	tgg	gga	1071
117	Met	Arg	Ala	Thr	Gln	Leu	Gln	Lys	Asn	Leu	Thr	Cys	Glu	Val	Trp	Gly	
118								320			325			330			
120	ccc	acc	tcc	cct	aag	ctg	atg	ctg	agc	ttg	aaa	ctg	gag	aac	aag	gag	1119
121	Pro	Thr	Ser	Pro	Lys	Leu	Met	Leu	Ser	Leu	Lys	Leu	Glu	Asn	Lys	Glu	
122								335			340			345			
124	gca	aag	gtc	tcg	aag	cgf	gag	aag	gcf	gtg	tgg	gtg	ctg	aac	cct	gag	1167
125	Ala	Lys	Val	Ser	Lys	Arg	Glu	Lys	Ala	Val	Trp	Val	Leu	Asn	Pro	Glu	
126								350			355			360			
128	gcf	ggg	atg	tgg	cag	tgt	ctg	agt	gac	tcg	gga	cag	gtc	ctg	ctg		1215
129	Ala	Gly	Met	Trp	Gln	Cys	Leu	Leu	Ser	Asp	Ser	Gly	Gln	Val	Leu	Leu	

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130	365	370	375	380	
132	gaa tcc aac atc aag gtt ctg ccc aca tgg tcc acc ccg gtg taa tgg				1263
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144	<213> ORGANISM: Human				
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153	20	25	30		
156	Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser Gln Lys Lys Ser				
157	35	40	45		
160	Ile Gln Phe His Trp Lys Asn Ser Asn Gln Ile Lys Ile Leu Gly Asn				
161	50	55	60		
164	Gln Gly Ser Ser Leu Thr Lys Gly Pro Ser Lys Leu Asn Asp Arg Ala				
165	65	70	75	80	
168	Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe Pro Leu Ile Ile				
169	85	90	95		
172	Arg Asn Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile Cys Glu Val Glu				
173	100	105	110		
176	Asp Gln Lys Glu Glu Val Gln Leu Leu Val Phe Gly Leu Thr Ala Asn				
177	115	120	125		
180	Ser Asp Thr His Leu Leu Gln Gly Gln Ser Leu Thr Leu Thr Leu Glu				
181	130	135	140		
184	Ser Pro Pro Gly Ser Ser Pro Ser Val Gln Cys Arg Ser Pro Arg Gly				
185	145	150	155	160	
188	Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser Val Ser Gln Leu Glu Leu				
189	165	170	175		
192	Gln Asp Ser Gly Thr Trp Thr Cys Thr Val Leu Gln Asn Gln Lys Lys				
193	180	185	190		
196	Val Glu Phe Lys Ile Asp Ile Val Val Leu Ala Phe Gln Lys Ala Ser				
197	195	200	205		
200	Ser Ile Val Tyr Lys Lys Glu Gly Glu Gln Val Asp Phe Ser Phe Pro				
201	210	215	220		
204	Leu Ala Phe Thr Val Glu Lys Leu Thr Gly Ser Gly Glu Leu Trp Trp				
205	225	230	235	240	
208	Gln Ala Glu Arg Ala Ser Ser Ser Lys Ser Trp Ile Thr Phe Asp Leu				
209	245	250	255		
212	Lys Asn Lys Glu Val Ser Val Lys Arg Val Thr Gln Asp Pro Lys Leu				
213	260	265	270		
216	Gln Met Gly Lys Lys Leu Pro Leu His Leu Thr Leu Pro Gln Ala Leu				
217	275	280	285		
220	Pro Gln Tyr Ala Gly Ser Gly Asn Leu Thr Leu Ala Leu Glu Ala Lys				
221	290	295	300		

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224 Thr Gly Lys Leu His Gln Glu Val Asn Leu Val Val Met Arg Ala Thr
 225 305 310 315 320
 228 Gln Leu Gln Lys Asn Leu Thr Cys Glu Val Trp Gly Pro Thr Ser Pro
 229 325 330 335
 232 Lys Leu Met Leu Ser Leu Lys Leu Glu Asn Lys Glu Ala Lys Val Ser
 233 340 345 350
 236 Lys Arg Glu Lys Ala Val Trp Val Leu Asn Pro Glu Ala Gly Met Trp
 237 355 360 365
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 264 <212> TYPE: DNA
 265 <213> ORGANISM: Artificial Sequence
 267 <220> FEATURE:
 268 <223> OTHER INFORMATION: sk 727/725
 270 <400> SEQUENCE: 4
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 274 <210> SEQ ID NO: 5
 275 <211> LENGTH: 48
 276 <212> TYPE: DNA
 277 <213> ORGANISM: Artificial Sequence
 279 <220> FEATURE:
 280 <223> OTHER INFORMATION: sk 727/725
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 288 <212> TYPE: DNA
 289 <213> ORGANISM: Artificial Sequence
 291 <220> FEATURE:
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 294 <400> SEQUENCE: 6
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 301 <213> ORGANISM: Artificial Sequence

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Input Set : A:\24577-cyb.ST25.txt
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 320 ctggcgctcc tcccagcagc cactcaggaa aagaaagtgg tgctggccaa aaaaggggat 180
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 334 aggagtccaa gggtaaaaaa catacagggg gggaaagaccc tctccgtgtc tcagctggag 600
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 370 tgttgtcttc tagttccag aggcttaatc acaccgtccct ccacgcccatt tcttttctt 1680
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 374 cc 1742
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 378 <211> LENGTH: 457
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 388 Ala Leu Leu Pro Ala Ala Thr Gln Gly Lys Lys Val Val Leu Gly Lys
 389 20 25 30
 392 Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser Gln Lys Lys Ser

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